WEST Search History

DATE: Thursday, August 21, 2003

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT; PLUR=YES; OP=AND		
L1	dam.clm.	3181	L1
L2	($methylase or methyltransferase$ or methyl-transferase$).clm.	241	L2
L3	L2 or dna.clm.	17060	L3
L4	L3 and l1	18	L4
L5	dam same (bacter$ or microorgan$ or salmonel$ or shigel$ or coli)	446	L5
L6	dam same (prokaryot$ or procaryot$)	13	L6
L7	L5 not l6 not l4	425	L7
L8	($methylase or methyltransferase$ or methyl-transferase$)	2250	L8
L9	L8 and l7	153	L9
L10	L9 and (heterologous or foreign or nonnative or recombinant or artificial or fusion)	152	L10
L11	L9 and (heterologous or foreign or nonnative or fusion)	121	L11
L12	L9 and (heterologous or foreign or nonnative or fusion)	121	L12
L13	($methylase or methyltransferase$ or methyl-transferase$ or dam) near50 (mutant or mutation or mutagenesis or alter$ or mutants or mutations or insertion or deletion or modification or modified or truncated or trucation)	1690	L13

L14	L13 and l5	106	L14

DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=AND

L15	dam.ti.	7503	L15
L16	L15 and dna	4	L16

END OF SEARCH HISTORY

05249481 86250633 PMID: 3522556

Mutant **of Salmonella typhimurium LT2 deficient in DNA adenine methylation.**

Ritchie L J; Hall R M; Podger D M

Journal of bacteriology (UNITED STATES) Jul 1986, 167 (1) p420-2, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A **mutant** of Salmonella typhimurium LT2 deficient in methylation of the adenine residues in the sequence 5'- **GATC** -3' was isolated. The **mutation** (dam-1) was linked to the cysG locus, and the properties of the **mutant** were similar to those of Escherichia coli dam **mutants** . Reversion of the hisC3076 frameshift **marker** by 9-aminoacridine was substantially enhanced by the dam-1 **mutation** , implying a direct role for adenine methylation in the prevention of frameshift **mutation** induction.

Descriptors: Adenine--metabolism--ME; *DNA, Bacterial--metabolism--ME; * **Mutation** ; *Salmonella typhimurium--genetics--GE; Aminacrine--pharmacology --PD; Genes, Bacterial; Methylation; Methyltransferases--genetics--GE; Methyltransferases--metabolism--ME; Salmonella typhimurium--metabolism--ME ; Site-Specific DNA-Methyltransferase (Adenine-Specific)

CAS Registry No.: 0 (DNA, Bacterial); 73-24-5 (Adenine); 90-45-9 (Aminacrine)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19860811

Record Date Completed: 19860811

10368256 96173077 PMID: 8589735

Adenine **methylation at dam sites increases transient gene expression in plant cells.**

Graham M W; Larkin P J

CSIRO Division of Plant Industry, Canberra, Australia.

Transgenic research (ENGLAND) Sep 1995, 4 (5) p324-31, ISSN 0962-8819 Journal Code: 9209120

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Escherichia coli encodes two major DNA methylation systems: dam, which produces 6-methyladenine; and dcm, which produces 5-methylcytosine. About 1-2% of **adenine** and cytosine residues in plasmid DNAs prepared in E. coli are methylated by these systems. Since DNA methylation profoundly influences gene expression in eukaryotes, we were interested in determining whether these bacterially encoded modifications might also effect plant gene expression in experimental systems. We therefore examined the influence of dam and dcm methylation on gene expression from four GUS fusion constructs in transient assays in protoplasts and microprojectile-bombarded whole tissues. In these constructs, GUS expression was driven by promoter regions derived from the Arabidopsis alcohol dehydrogenase (Adh1), maize ubiquitin (Ubi1), rice actin (Act1) and CaMV 35S genes. We show that methyladenine produced by dam methylation increased gene expression from constructs based on the Adh1, Ubi1 and Act1 genes. The increase in gene expression ranged from three-fold for Ubi1 and Adh1 in protoplasts to 50-fold for Act1 in bombarded wheat tissues. Expression of a 35S.GUS construct was, however, insensitive to dam methylation. dcm methylation had little if any effect on transient gene expression for any of these constructs. We provide indirect evidence that the critical sites of **adenine** methylation lie within sequences from the promoter regions, suggesting that dam methylation increases transcription rate. These results have important experimental implications and also raise the intriguing possibility that methyladenine might play a role in the regulation of gene expression in vivo.

Descriptors: **Adenine** --metabolism--ME; *Gene Expression Regulation, Plant; *Plants--genetics--GE; *Plants--metabolism--ME; Binding Sites; DNA Modification Methylases--metabolism--ME; Escherichia coli--metabolism--ME; Methylation; Plants--cytology--CY; Plants, Genetically Modified; Promoter Regions (Genetics); Recombinant Fusion Proteins--chemistry--CH; Recombinant Fusion Proteins--genetics--GE

CAS Registry No.: 0 (Recombinant Fusion Proteins); 73-24-5 (Adenine)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases)

Gene Symbol: Act1; Adh1; GUS; Ubi1

Record Date Created: 19960327

Record Date Completed: 19960327

06954574 91195052 PMID: 2014170

Molecular cloning and characterization of the gene encoding the adenine **methyltransferase M.CviRI from Chlorella virus XZ-6E.**

Stefan C; Xia Y N; Van Etten J L

Department of Plant Pathology, University of Nebraska, Lincoln 68583-0722.

Nucleic acids research (ENGLAND) Jan 25 1991, 19 (2) p307-11, ISSN 0305-1048 Journal Code: 0411011

Contract/Grant No.: GM-32441; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The gene encoding the DNA methyltransferase M.CviRI from Chlorella virus XZ-6E was cloned and expressed in Escherichia coli. M.CviRI methylates **adenine** in TGCA sequences. DNA containing the M.CviRI gene was sequenced and a single open reading frame of 1137 bp was identified which could code for a polypeptide of 379 amino acids with a predicted molecular weight of 42,814. Comparison of the M.CviRI predicted amino acid sequence with another Chlorella virus and 14 bacterial **adenine** methyltransferases revealed extensive similarity to the other Chlorella virus enzyme.

Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: Chlorella; *DNA Modification Methylases--genetics--GE; *Site-Specific DNA-Methyltransferase (**Adenine** -Specific)--genetics--GE; *Viruses--enzymology--EN; Amino Acid Sequence; Base Sequence; Cloning, Molecular; Escherichia coli--genetics--GE; Gene Expression Regulation, Bacterial; Gene Expression Regulation, Enzymologic; Genes, Bacterial; Molecular Sequence Data; Nucleic Acid Hybridization; Plasmids; Sequence Alignment

Molecular Sequence Databank No.: GENBANK/M38173; GENBANK/X56859; GENBANK/X56860; GENBANK/X56861; GENBANK/X56862; GENBANK/X56863; GENBANK/X56864; GENBANK/X56865; GENBANK/X57509; GENBANK/X57510

CAS Registry No.: 0 (Plasmids)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 2.1.1.- (DNA modification methylase CviRI); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (**Adenine** -Specific))

Gene Symbol: M.CviRI

Record Date Created: 19910513

Record Date Completed: 19910513

06883099 91123209 PMID: 1846861

Two-step cloning and expression in Escherichia coli of the DNA restriction-modification system StyLTI of Salmonella typhimurium.

De Backer O; Colson C

Departement de Biologie, Universite Catholique de Louvain, Louvain-la-Neuve, Belgium.

Journal of bacteriology (UNITED STATES) Feb 1991, 173 (3) p1321-7, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The StyLTI restriction-modification system is common to most strains of the genus Salmonella, including Salmonella typhimurium. We report here the two-step cloning of the genes controlling the StyLTI system. The StyLTI methylase gene (mod) was cloned first. Then, the companion endonuclease gene (res) was introduced on a compatible vector. A strain of S. typhimurium sensitive to the coliphage lambda was constructed and used to select self-modifying recombinant phages from a Res- Mod+ S. typhimurium genomic library in the lambda EMBL4 cloning vector. The methylase gene of one of these phages was then subcloned in pBR328 and transferred into Escherichia coli. In the second step, the closely linked endonuclease and methylase genes were cloned together on a single DNA fragment inserted in pACYC184 and introduced into the Mod+ E. coli strain obtained in the first step. Attempts to transform Mod- E. coli or S. typhimurium strains with this Res+ Mod+ plasmid were unsuccessful, whereas transformation of Mod+ strains occurred at a normal frequency. This can be understood if the introduction of the StyLTI genes into naive hosts is lethal because of degradation of host DNA by restriction activity; in contrast to most restriction-modification systems, StyLTI could not be transferred into naive hosts without killing them. In addition, it was found that strains containing only the res gene are viable and lack restriction activity in the absence of the companion mod gene. This suggests that expression of the StyLTI endonuclease activity requires at least one polypeptide involved in the methylation activity, as is the case for types I and III restriction-modification systems but not for type II systems.

Tags: Support, Non-U.S. Gov't

Descriptors: DNA Modification Methylases--genetics--GE; *DNA Restriction Enzymes--genetics--GE; *Deoxyribonucleases, Type III Site-Specific --genetics--GE; *Escherichia coli--genetics--GE; *Gene Expression Regulation, Bacterial; *Salmonella typhimurium--genetics--GE; *Site-Specific DNA-Methyltransferase (**Adenine** -Specific)--genetics--GE; Cloning, Molecular; DNA Modification Methylases--metabolism--ME; DNA Restriction Enzymes--metabolism--ME; Deoxyribonucleases, Type III Site-Specific--metabolism--ME; Genes, Bacterial; Phenotype; Plasmids; Restriction Mapping; Salmonella typhimurium--enzymology--EN; Site-Specific DNA-Methyltransferase (**Adenine** -Specific)--metabolism--ME; Transformation, Bacterial

CAS Registry No.: 0 (Plasmids)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 2.1.1.- (DNA modification methylase StyLTI); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (**Adenine** -Specific)); EC 3.1.21 (DNA Restriction Enzymes); EC 3.1.21.- (endodeoxyribonuclease StyLTI); EC 3.1.21.5 (Deoxyribonucleases, Type III Site-Specific)

Gene Symbol: mod; res

Record Date Created: 19910311

Record Date Completed: 19910311

06560016 90185237 PMID: 2155857

DNA methylation in Neisseria gonorrhoeae and other Neisseriae.

Ritchot N; Roy P H

Departement de Biochimie, Faculte des Sciences et de Genie, Universite Laval, Sainte-Foy, Canada.

Gene (NETHERLANDS) Jan 31 1990, 86 (1) p103-6, ISSN 0378-1119 Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

It has been reported in the literature that Neisseria gonorrhoeae DNA is modified by the methyltransferases (MTases) M.NgoI, M.NgoII, and M.NgoIII, as well as three other cytosine MTases and one **adenine** MTase, even if the corresponding restriction endonucleases are not present. We envisioned the possibility of cloning one of the N. gonorrhoeae MTase-encoding genes for use as a species-specific DNA probe. We therefore undertook a survey of methylation patterns of several clinical isolates of N. gonorrhoeae and N. meningitidis as well as ATCC strains of other Neisseriae. We found, from digestion patterns with isoschizomers, one N. gonorrhoeae strain that lacked M.NgoII and two that lacked M.NgoIII. All N. meningitidis strains (save one) were resistant to digestion with NlaIV thus possessing an MTase like NgoV, and one was resistant to SstII, thus having an NgoIII-like MTase. None were resistant to isoschizomers of NgoI, NgoIII and NgoIV. Some other Neisseriae had an MTase with NlaIV (NgoV) specificity, but none had NgoI, II, III or IV specificity, except for the Branhamella-like N. caviae-ovis group and N. lactamica where these specificities were present in at least one strain of this group. Therefore, among the Neisseriae other than N. caviae only M.NgoI is N. gonorrhoeae-specific.

Descriptors: *DNA Modification Methylases--metabolism--ME; *Neisseria --genetics--GE; *Neisseria gonorrhoeae--genetics--GE; DNA Restriction Enzymes--metabolism--ME; DNA, Bacterial--metabolism--ME; Methylation; Neisseria--enzymology--EN; Neisseria gonorrhoeae--enzymology--EN

CAS Registry No.: 0 (DNA, Bacterial)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19900426

Record Date Completed: 19900426

06316635 89332822 PMID: 2667217

The great GATC: DNA methylation in E. coli.

Barras F; Marinus M G

Trends in genetics - TIG (ENGLAND) May 1989, 5 (5) p139-43, ISSN 0168-9525 Journal Code: 8507085

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

In Escherichia coli the methylation of the **adenine** in the sequence 5'-GATC-3' is catalysed by the dam gene product, a DNA **adenine** methylase. We review the proposed roles for this methylation, and the sequence it modifies, in mismatch repair, DNA-protein interaction, gene expression, the initiation of chromosome replication, chromosome segregation, chromosome structure and the occurrence of mutational hotspots. (27 Refs.)

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *DNA Modification Methylases--metabolism--ME; *DNA, Bacterial--metabolism--ME; *Escherichia coli--genetics--GE; Base Sequence; Chromosomes, Bacterial; DNA Replication; DNA, Bacterial--genetics--GE; Gene Expression Regulation; Methylation

CAS Registry No.: 0 (DNA, Bacterial)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases)

Record Date Created: 19890829

Record Date Completed: 19890829

DNA adenine methylase mutants of Salmonella typhimurium and a novel dam-regulated locus.

Torreblanca J ; Casadesus J
Departamento de Genetica, Facultad de Biologia, Universidad de Sevilla, Spain.

Genetics (UNITED STATES) Sep 1996, 144 (1) p15-26, ISSN 0016-6731
Journal Code: 0374636
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Mutants of Salmonella typhimurium lacking DNA adenine methylase were isolated; they include insertion and deletion alleles. The dam locus maps at 75 min between cysG and aroB, similar to the Escherichia coli dam gene. Dam- mutants of S. typhimurium resemble those of E coli in the following phenotypes: (1) increased spontaneous mutations, (2) moderate SOS induction, (3) enhancement of duplication segregation, (4) inviability of dam recA and dam recB mutants, and (5) suppression of the inviability of the dam recA and dam recB combinations by mutations that eliminate mismatch repair. However, differences between S. typhimurium and E. coli dam mutants are also found: (1) S. typhimurium dam mutants do not show increased UV sensitivity, suggesting that methyl-directed mismatch repair does not participate in the repair of UV-induced DNA damage in Salmonella. (2) S. typhimurium dam recJ mutants are viable, suggesting that the Salmonella RecJ function does not participate in the repair of DNA strand breaks formed in the absence of Dam methylation. We also describe a genetic screen for detecting novel genes regulated by Dam methylation and a locus repressed by Dam methylation in the S. typhimurium virulence (or "cryptic") plasmid.

Tags: Support, Non-U.S. Gov't
Descriptors: *Salmonella typhimurium--enzymology--EN; *Site-Specific DNA-Methyltransferase (Adenine-Specific)--genetics--GE; Chromosome Mapping; Cloning, Molecular; DNA Methylation; DNA Transposable Elements; Gene Deletion; Genetic Complementation Test; Mutagenesis, Insertional; Salmonella typhimurium--genetics--GE; Salmonella typhimurium--radiation effects--RE; Site-Specific DNA-Methyltransferase (Adenine-Specific) --metabolism--ME; Ultraviolet Rays
CAS Registry No.: 0 (DNA Transposable Elements)
Enzyme No.: EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))
Record Date Created: 19970128

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File 155:MEDLINE(R)  1966-2003/Aug W3
       (c) format only 2003 The Dialog Corp.
*File 155: Medline has been reloaded and accession numbers have
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S4         137   S2 NOT S3
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?e adenine methylase

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E3         0      *ADENINE METHYLASE
E4         0    1  ADENINE NUCLEOTIDE TRANSLOCASE
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E6         1       ADENINE NUCLEOTIDE TRANSLOCATOR 1 --ANTAGONIST
E7         3       ADENINE NUCLEOTIDE TRANSLOCATOR 1 --BIOSYNTHES
E8        10       ADENINE NUCLEOTIDE TRANSLOCATOR 1 --GENETICS -
E9         5       ADENINE NUCLEOTIDE TRANSLOCATOR 1 --METABOLISM
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E12        1       ADENINE NUCLEOTIDE TRANSLOCATOR 2 --BIOSYNTHES

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?e adenine methyltransferase

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E3         0      *ADENINE METHYLTRANSFERASE
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E6         1       ADENINE NUCLEOTIDE TRANSLOCATOR 1 --ANTAGONIST
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E6        35       DEOXYADENINE NUCLEOTIDES --ANALYSIS --AN
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E8         8       DEOXYADENINE NUCLEOTIDES --BIOSYNTHESIS --BI
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E7         1  METHYLASPARAGINAMIDE
E8        10  METHYLASPARAGINE
E9         1  METHYLASPARAGINES
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E12       21  METHYLASPARTASE

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           40430  ADENINE?
      S7      43  S6 AND ADENINE?
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S2         182   S1 AND (MUTANT? OR MUTATION? OR MUTAGEN? OR ALTER? OR MODI-
                   FICA? OR HETEROLOGO?)
S3          45   S2/1999:2003
S4         137   S2 NOT S3
S5          19   S4 AND (FOREIGN? OR HETEROLOG? OR NONNATIVE? OR FUSION? OR
                   ANTIBIOT? OR MARKER?)
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              13  S9
     S10      30  S8 NOT S9
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06237073 89252867 PMID: 3074010

The DNA and S-adenosylmethionine-binding regions of EcoDam and related methyltransferases.

Guschlbauer W

Departement de Biologie, Centre d'Etudes Nucleaires de Saclay, Gif-sur-Yvette, France.

Gene (NETHERLANDS) Dec 25 1988, 74 (1) p211-4, ISSN 0378-1119 Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Previous comparison of the amino acid sequences of the GATC-methylating Escherichia coli Dam methyltransferase (MTase) with those of other **adenine** MTases (M.EcoRV, M.DpnII and T4Dam) localized four conserved regions. Regions III and IV have similarities with many other MTases. The sequence DPPY (or NPPY) is always present in region IV. It was suggested to be the AdoMet binding site. Publication of the nucleotide and amino acid sequences of M.CviBIII, M.DpnA and MutH give further credence to this assignment: M.DpnA, which also methylates GATC, has strong similarities with regions III and IV; M.CviBIII, a cytosine methylase, has a characteristic NPPY sequence in region IV, and only limited resemblance in region III; MutH, the GATC-specific endonuclease in DNA mismatch repair, has significant similarities uniquely in region III. The presently available evidence suggests that region III is the GAT(C) binding site and region IV is the AdoMet binding site. This hypothesis is strengthened by recent genetic findings.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--metabolism--ME; *DNA Modification Methylases--metabolism--ME; *DNA, Bacterial--metabolism--ME; *Escherichia coli--enzymology--EN; *Methyltransferases--metabolism--ME; *S-Adenosylmethionine--metabolism--ME; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Binding Sites; DNA Modification Methylases--genetics--GE; DNA Repair; Endodeoxyribonucleases--genetics--GE; Methyltransferases--genetics--GE; Molecular Sequence Data; Protein Binding; Protein Conformation; Sequence Homology, Nucleic Acid

CAS Registry No.: 0 (Bacterial Proteins); 0 (DNA, Bacterial); 29908-03-0 (S-Adenosylmethionine)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.- (DNA Modification Methylases); EC 2.1.1.- (Dam methyltransferase); EC 3.1.- (Endodeoxyribonucleases); EC 3.1.21.- (MutH gene product)

Record Date Created: 19890626

10502670 96313243 PMID: 8759008

Cloning and analysis of the genes encoding the type IIS restriction-modification system HphI from Haemophilus parahaemolyticus.

Lubys A; Lubiene J; Kulakauskas S; Stankevicius K; Timinskas A; Janulaitis A

Institute of Biotechnology, Vilnius, Lithuania.

Nucleic acids research (ENGLAND) Jul 15 1996, 24 (14) p2760-6, ISSN 0305-1048 Journal Code: 0411011

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The genomic region encoding the type IIS restriction-modification (R-M) system HphI (enzymes recognizing the asymmetric sequence 5'-GGTGA-3'/5'-TCACC-3') from Haemophilus parahaemolyticus were cloned into Escherichia coli and sequenced. Sequence analysis of the R-M HphI system revealed three adjacent genes aligned in the same orientation: a cytosine 5 methyltransferase (gene hphIMC), an **adenine** N6 methyltransferase (hphIMA) and the HphI restriction endonuclease (gene hphIR). Either methyltransferase is capable of protecting plasmid DNA in vivo against the action of the cognate restriction endonuclease. hphIMA methylation renders plasmid DNA resistant to R.Hindill at overlapping sites, suggesting that the **adenine** methyltransferase modifies the 3'-terminal A residue on the GGTGA strand. Strong homology was found between the N-terminal part of the m6A methyltransferasease and an unidentified reading frame interrupted by an incomplete gaIE gene of Neisseria meningitidis. The HphI R-M genes are flanked by a copy of a 56 bp direct nucleotide repeat on each side. Similar sequences have also been identified in the non-coding regions of H.influenzae Rd DNA. Possible involvement of the repeat sequences in the mobility of the HphI R-M system is discussed.

Descriptors: *DNA Modification Methylases--genetics--GE; *Deoxyribonucleases, Type II Site-Specific--genetics--GE; *Haemophilus--enzymology--EN; Amino Acid Sequence; Base Sequence; Cloning, Molecular; DNA Modification Methylases--metabolism--ME; DNA, Bacterial; Deoxyribonucleases, Type II Site-Specific--metabolism--ME; Escherichia coli; Genetic Vectors; Haemophilus--genetics--GE; Molecular Sequence Data; Substrate Specificity

Molecular Sequence Databank No.: GENBANK/X85374

CAS Registry No.: 0 (DNA, Bacterial); 0 (Genetic Vectors)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 3.1.21.- (endodeoxyribonuclease HphI); EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific)

Record Date Created: 19960917

Record Date Completed: 19960917

10469038 96276208 PMID: 8693028

Electrotransformation of highly DNA-restrictive corynebacteria with synthetic DNA.

Ankri S; Reyes O; Leblon G

Institut de Genetique et Microbiologie, Universite de Paris-Sud, Orsay, France.

Plasmid (UNITED STATES) Jan 1996, 35 (1) p62-6, ISSN 0147-619X Journal Code: 7802221

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Highly DNA-restrictive Corynebacteria can be transformed with DNA made in vitro by PCR amplification of a sequence that contains the replication origin of pBL1, a plasmid common to many Corynebacteria. In all strains examined, the transformation efficiencies of PCR-synthetized DNA equal or improve the performances of heterologous DNA extracted from wild-type and dam(-)-dcm-strains of Escherichia coli. The transformation efficiencies obtained with PCR-made DNA may be high enough to permit its general application to experiments of gene integration.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Corynebacterium--genetics--GE; *DNA Restriction Enzymes --metabolism--ME; *DNA, Bacterial--genetics--GE; *DNA, Recombinant --genetics--GE; *Plasmids--genetics--GE; *Transformation, Bacterial; Corynebacterium--enzymology--EN; DNA Modification Methylases--genetics--GE; DNA Modification Methylases--metabolism--ME; Electroporation; Escherichia coli--genetics--GE; Methylation; Polymerase Chain Reaction; Site-Specific DNA-Methyltransferase (**Adenine** -Specific)--genetics--GE; Site-Specific DNA-Methyltransferase (**Adenine** -Specific)--metabolism--ME

CAS Registry No.: 0 (DNA, Bacterial); 0 (DNA, Recombinant); 0 (Plasmids)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (**Adenine** -Specific)); EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19960829

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Chlorella virus NY-2A encodes at least 12 DNA endonuclease/methyltransferase genes.

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Document type: Journal Article

Languages: ENGLISH

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The 380-kb chlorella virus NY-2A genome is highly methylated; 45% of the cytosines are 5-methylcytosine (5mC) and 37% of the **adenines** are N6-methyladenine (6mA). Based on the sensitivity/resistance of NY-2A DNA to 80 methylation-sensitive DNA restriction endonucleases, the virus is predicted to encode at least 10 DNA methyltransferases: 7 6mA-specific methyltransferases, M.CviQI (GTmAC), M.CvQII (RmAR), M.CviQIII (TCGmA), M.CviQIV (GmATC), M.CviQV (TGCmA), M.CviQVI (GmANTC), and M.CviQVII (CmATG): and 3 5mC-specific methyltransferases, M.CviQVIII [RGmC(T/C/G)], M.CviQIX (mCC), and M.CviQX (mCGR). Five of the 6mA methyltransferase genes, M.CviQI, M.CviQIII, M.CviQV, M.CviQVI, and M.CviQVII, were cloned and sequenced. In addition, 2 site-specific endonuclease activities, R.CviQI (G/TAC) and NY2A-nickase (R/AG), were detected in cell-free extracts from NY-2A virus-infected chlorella. Therefore, the NY-2A genome contains at least 12 DNA methyltransferase and endonuclease genes which, altogether, compose about 3-4% of the virus genome.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Chlorella--virology--VI; *DNA Modification Methylases --genetics--GE; *Deoxyribonuclease I--genetics--GE; *Phycodnaviridae --genetics--GE; Amino Acid Sequence; DNA Methylation; DNA Modification Methylases--isolation and purification--IP; Deoxyribonuclease I--isolation and purification--IP; Genes, Viral--genetics--GE; Molecular Sequence Data; Phycodnaviridae--enzymology--EN; Sequence Alignment; Sequence Homology, Amino Acid

Molecular Sequence Databank No.: GENBANK/AF021248; GENBANK/AF021249; GENBANK/AF021250; GENBANK/AF021251; GENBANK/AF021252

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 3.1.21.1 (Deoxyribonuclease I)

Record Date Created: 19980220

Record Date Completed: 19980220

these leaky mutants retain endonucleolytic activity; strong binding, without cleavage, to all EcoRI sites in the E. coli genome is likely to be toxic. It is likely that leaky mutants can be expressed in cells that also express the EcoRI methylase activity so that the proteins can be characterized. Leaky mutants that lack nuclease activity or EcoRI-delN29 could be used as an initial DBP for DNA targets related to the EcoRI sequence. The non-binding mutants, AT139, GS140, and RQ203, could also be used as initial DBPs; alterations or extension of the protein in such a way that additional base pairs are contacted will supply the free-energy lost through these mutations. Yanofsky et al. state that most null mutants of EcoRI accessible through hydroxylamine have probably been identified. Other mutants are likely to be revealed by other mutagens. Null mutants are, however, selected not only for lack of nuclease activity, but also for non-binding, and therefore are not so useful as leaky mutants.

Detailed Description Text (383):
First, each enzyme that has a unique possible site is picked; if two of these overlap, then the better enzyme is picked. An enzyme is better if it: a) generates cohesive ends, b) has unambiguous recognition, c) has higher specific activity, or d) (for work in E. coli) is not sensitive to dam or dcm methylation. Next, those sites close to other sites already picked are eliminated because many sites very close together are not useful. Finally, sites are chosen to minimize the size of the longest piece between restriction sites.

☐ 92. Document ID: US 5194387 A

L14: Entry 92 of 106 File: USPT Mar 16, 1993

DOCUMENT-IDENTIFIER: US 5194387 A
TITLE: Process for the incorporation of DNA molecules into microorganisms with methyl-specific restriction systems

Brief Summary Text (2):
The introduction of foreign DNA, including plasmids, phages, and chromosomal DNA fragments, into microorganisms is a well established procedure. However, certain microorganisms cleave and inactivate foreign DNA through restriction systems making it difficult or impossible to introduce foreign DNA into these microorganisms. Restriction-modification systems are widespread in microorganisms. Most restriction-modification systems are composed of a methylase and an endonuclease. The modification enzyme (methylase) modifies the host DNA at a specific sequence composed of 4 or more bases, and the restriction endonuclease cleaves unmodified, foreign DNA at or near the specific sequence (for a review see Kessler et al. Gene 47 pg. 1-153 (1986)). Over 600 restriction endonucleases and 98 methylases are known. Three methyl-specific restriction systems have been described. In strains with methyl-specific restriction systems, foreign, methyl modified DNA is restricted and the host "modification" is the lack of modified DNA. Diplococcus pneumoniae restricts DNA containing N.sup.6 -methyladenine at the sequence GATC. Two other strains restrict DNA containing 5-methylcytosine, but these strains show little or no sequence specificity.

Brief Summary Text (15):
The restriction shown by S. avermitilis is not limited to DNA isolated from E. coli, but also restricts DNA from a modification proficient Streptomyces. This was determined by isolating DNA from S. griseus. S. griseus is a known host for pVE1 derivatives, although it restricts the entry of DNA from S. avermitilis and S. lividans (see Table 3). When S. griseus was transformed with pVE28, only a derivative, which was 0.4 kb smaller than pVE28, was isolated from the transformants. This deletion derivative was designated pVE614. When pVE614 is isolated from S. griseus it is resistant to cleavage by SstI. However, when pVE614 is isolated from S. lividans, it is cleaved by SstI at a single site, the parental plasmid pVE28 contains two SstI sites, but one site is within the 0.4 kb region deleted to form pVE614. Evidently, S. griseus contains a restriction-modification system which modifies the DNA that overlaps the SstI site. When pVE614 was isolated from S. griseus it could be used to transform S. lividans, but not S. avermitilis. This was due to restriction, rather than problems with the maintenance or replication of pVE614, because pVE614 DNA isolated from S. lividans will efficiently transform S. avermitilis (see Table 3). Thus, S. avermitilis contains a restriction system which restricts the entry of DNA from E. coli RR1, known to contain the dam and dcm modification systems, and from S. griseus, shown here to modify DNA at or near a SstI site in pVE614

Detailed Description Text (2):
Since S. avermitilis does not restrict DNA isolated from S. lividans, S. lividans must process DNA in one of two ways so that DNA is not cleaved by S. avermitilis restriction enzymes. S. lividans, a species unrelated to S. avermitilis, could coincidently modify the sites in DNA recognized by a S. avermitilis restriction-modification system. Alternatively, S. avermitilis might contain a methyl-specific restriction system and S. lividans might not methylate DNA. This latter possibility was tested by transforming S. avermitilis protoplasts with pVE28, a 4.9 kb, high copy number Streptomyces plasmid that was modified in vitro with various methylases. Table 4 shows that S. avermitilis strongly restricted DNA that was modified with AluI, dam, HhaI, HphI, and TagI methylases, the efficiency of transformation (eot was reduced between 10.sup.-3 and 10.sup.-4. The 4 or 5 bp recognition sites for these methylases occur frequently in the DNA tested. pVE28 and other pVE1 derivatives with only 1, 2, or 3 sites for in vitro methylation were only weakly restricted since their efficiency of transformation was reduced only about 10 fold (see Table 4). This indicates that the probability of a DNA molecule being restricted by S. avermitilis is proportional to the number of methylated bases it contains. There appears to be no sequence specificity to the methyl-specific restriction observed in S. avermitilis, since all 8 methylases tested reduced the eot of the modified plasmids. S. avermitilis restricts both 5 -methylyctosine and N.sup.6 methyladenine modified DNA.

Detailed Description Text (4):
E. coli RR1, the host for the shuttle vectors in Table 2, contains two DNA methylases. The dcm product modifies the sequence GG(AT)CC to produce 5-methylyctosine and the dam product modifies the sequence GATC yielding N.sup.6 -methyladenine. As shown above, S. avermitilis restricts modified DNA, this could explain why S. avermitilis can not be transformed by shuttle vectors isolated from E. coli RR1. To test if the dcm and dam modifications cause S. avermitilis to restrict shuttle vectors isolated from E. coli, shuttle vectors were isolated from a methylase deficient E. coli GM272 (dcm,dam,hsd). As Table 5 shows, DNA from GM272 could be transformed directly into S. avermitilis. However, the plasmids isolated from GM272 still showed a reduced efficiency of transformation compared to plasmids isolated from Streptomyces. The residual restriction of DNA isolated from GM272 may be because the dam and dcm mutations in GM272 do not completely eliminate all DNA methylation. This was tested by comparing the restriction enzyme digestion pattern of shuttle vector DNA isolated from GM272 and Streptomyces which had been cleaved with methylation sensitive enzymes. When pVE3 and pVE328 DNAs isolated from GM272 were cleaved with MboI and EcoRII, faint bands resulting from only partial cleavage were visible. In contrast, the shuttle vectors DNAs isolated from Streptomyces were cleaved to completion. Thus, it is likely the restriction seen when DNA from GM272 is introduced into S. avermitilis is the result of the residual methylase activity in GM272.

recombination in lacZ (Konrad, E. B. 1977. J. Bacteriol. 130:167-172). No demonstration of RecA-independent microhomologous recombination in vitro has been reported.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 89. Document ID: US 5202256 A

L14: Entry 89 of 106 File: USPT Apr 13, 1993

DOCUMENT-IDENTIFIER: US 5202256 A
TITLE: Bioadhesive precursor protein expression vectors

Detailed Description Text (137):
An in-frame gene fusion between the trpB portion of pGX2346, and the bioadhesive precursor protein cDNA of pGX2368 is constructed in the following manner: A BclI endonuclease recognition site was first placed at the translation stop codon of pGX2368 by changing two bases as indicated in FIG. 1 using oligonucleotide-directed mutagenesis (Zoller, M. J. and M. Smith, Methods Enzymol., 100:457-500, 1983) to create plasmid pGX2380. Both plasmids pGX2380 and pGX2346 are grown for DNA preparation in an E. coli host that contains the dam mutation (defective in DNA adenine methylase) so that they could be digested with BclI. The non-methylated pGX2346 DNA is cut with NotI and the pGX2380 DNA is cut with XbaI. Then both DNAs are treated with E. coli DNA polymerase (Klenow fragment) to fill in the 5' single-stranded DNA overhangs. The DNAs are then ligated at high DNA concentration (approximately 2 ug of each DNA in 20 ul) with T4 ligase. The ligation product is cut with BclI then ligated again at low DNA concentration (approximately 1 ug total DNA in 150 ul volume) and used to transform E. coli GX3015. A transformant with the desired construction (see FIG. 6) is designated pGX2383. GX3015 cells with plasmid pGX2383 produce a bioadhesive precursor protein of approximately 24,000 M.W. upon induction of the hybrid lambda promoter by a shift of growth temperature from 32.degree. to 37.degree. C.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc
Image

☐ 90. Document ID: US 5202236 A

L14: Entry 90 of 106 File: USPT Apr 13, 1993

DOCUMENT-IDENTIFIER: US 5202236 A
TITLE: Method of producing bioadhesive protein

Detailed Description Text (138):
An in-frame gene fusion between the trpB portion of pGX2346, and the bioadhesive precursor protein cDNA of pGX2368 is constructed in the following manner: A BclI endonuclease recognition site was first placed at the translation stop codon of pGX2368 by changing two bases as indicated in FIG. 1 using oligonucleotide-directed mutagenesis (Zoller, M. J. and M. Smith, Methods Enzymol., 100:457-500, 1983) to create plasmid pGX2380. Both plasmids pGX2380 and pGX2346 are grown for DNA preparation in an E. coli host that contains the dam mutation (defective in DNA adenine methylase) so that they could be digested with BclI. The non-methylated pGX2346 DNA is cut with NotI and the pGX2380 DNA is cut with XbaI. Then both DNAs are treated with E. coli DNA polymerase (Klenow fragment) to fill in the 5' single-stranded DNA overhangs. The DNAs are then ligated at high DNA concentration (approximately 2 ug of each DNA in 20 ul) with T4 ligase. The ligation product is cut with BclI then ligated again at low DNA concentration (approximately 1 ug total DNA in 150 ul volume) and used to transform E. coli GX3015. A transformant with the desired construction (see FIG. 6) is designated pGX2383. GX3015 cells with plasmid pGX2383 produce a bioadhesive precursor protein of approximately 24,000 M.W. upon induction of the hybrid lambda promoter by a shift of growth temperature from 32.degree. to 37.degree. C.

☐ 91. Document ID: US 5198346 A

L14: Entry 91 of 106 File: USPT Mar 30, 1993

DOCUMENT-IDENTIFIER: US 5198346 A
TITLE: Generation and selection of novel DNA-binding proteins and polypeptides

Detailed Description Text (37):
Most strains of E. coli contain the dam and dcm DNA-methylating systems. The Dam methylase transfers a methyl from S-adenosylmethionine (SAM) to the N.sub.6 of adenine residues in the subsequence GATC. The Dcm methylase transfers a methyl from SAM to the internal cytosine in the sequences CCAGG and CCTGG. If a DBP is desired that will bind to unmethylated DNA, and if the target sequence contains either the Dam or Dcm recognition sequence, then a Dam.sup.- or Dcm.sup.- strain should be used.

Detailed Description Text (215):
Yanofsky et al. (YAN087) report a number of mutants of EcoRI obtained by mutagenesis of a plasmid-borne gene with hydroxylamine and expression in cells lacking the EcoRI methylase activity. The initial gene comprises the lacUV5 promoter and a coding region that codes on expression for the EcoRI endonuclease. Three of the mutants could be expressed at high levels and were shown to be dimeric, viz. AT139, GS140, and RQ203; these mutations prevent protein-DNA binding. Other mutants (viz. LF46, RQ56, GE129, AT142, GE210, and SL259) of the ecoRI gene were obtained that were "leaky", i.e. they were lethal if induced with 1.0 mM IPTG. (This level of IPTG induces lacUV5 to the maximum extent.) The authors do not report whether

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DOCUMENT-IDENTIFIER: US 5849305 A
TITLE: Construction of Pasteurella haemolytica vaccines

Abstract Text (1):
Methylation of DNA can be a critical step in the introduction of DNA into P. haemolytica. A methyltransferase has been isolated and molecularly cloned for this purpose. Use of the methyltransferase has allowed construction of defined, attenuated mutants for use as vaccines to protect cattle.

Detailed Description Text (39):
After digestion with PhaI and transformation of AP1-200-9 strain of E. coli, fifteen cosmid clones of P. haemolytica genomic DNA were tested for endonuclease activity. The nine clones which were endonuclease-positive were tested for PhaI methyltransferase activity. All nine expressed methyltransferase activity in addition to endonuclease activity, as evidenced by resistance to digestion by PhaI of genomic DNA recovered from transformed E. coli. The selective recovery of clones containing functional methyltransferase was due to previous digestion of the cosmid library with PhaI prior to transformation of E. coli. Recovery of clones containing both PhaI endonuclease and methyltransferase activity is not surprising since restriction and modification enzymes have previously been shown to be closely linked (the proximity of such genes has obvious implications to gene inheritance arid the survival of the organism). The AP1-200-9 strain of E. coli (used to screen the cosmid library in this experiment) was designed by Piekarowicz et al., to give color selection for DNA-modifying enzymes (genes). The mrr and mcr systems, with a temperature-sensitive phenotype, induce inducible locus of the SOS response allows for color selection. All the transformants were blue after incubation at the permissive temperature for the mcr/mrr systems. Recovery of clones containing both PhaI endonuclease and methyltransferase activity is not surprising since restriction and modification enzymes have previously been shown to be closely linked (the proximity of such genes has obvious implications to gene inheritance and to the survival of the organism). (Wilson et al., Annu. Rev. Genet. 25:585-627 (1991).)

Detailed Description Text (50):
The possibility that a system similar to E. coli mcr, mrr, is active in P. haemolytica was investigated by passage of pPh.DELTA.roACm.sup.R pD80 through E. coli strain GM2163 previously transformed with the recombinant cosmid containing PhaI methyltransferase (Raleigh et al., Proc. Natl. Acad. Sci. 83:9070-9074 (1986)). Since strain GM2163 is dam-, the resultant DNA would only be modified at PhaI sites (Marinus et al., Mol. Gen. Genet. 192:288-289 (1983)). Efficiency of transformation with this DNA, however, was not substantially different than that using DNA obtained from PhaI Mtase which is dam-methylated (Table 1). It is possible a second restriction system, not readily detectable in cell extracts, is active in P. haemoytica A1. Genes have been described in Neisseria gonnorhea MS11 which encode for restriction enzymes which are expressed at levels too low to detect biochemically (Stein et al., J. Bact. 74:4899-4906 (1992).

Detailed Description Text (62):
Construction of a P. haemolytica aroA mutant. The deletion plasmid, pPh.DELTA.aroACm.sup.R (Table 2), was constructed from pPharoA2 as described above and amplified in E. coli containing a cosmid clone carrying the PhaI methyltransferase gene on a 20-kb P. haemolytica DNA fragment. Although resistant to PhaI endonuclease digestion, introduction of pPh.DELTA.aroACm.sup.R into P. haemolytica strain NADC-D60 by electroporation failed to generate Cm resistant colonies. The inability to transform P. haemolytica with pPh.DELTA.aroACm.sup.R suggested that plasmids containing a Co1E1 origin do not replicate in this bacterium.

Detailed Description Text (64):

WEST Search History

DATE: Thursday, August 21, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=AND			
L1	dam.clm.	3181	L1
L2	($methylase or methyltransferase$ or methyl-transferase$).clm.	241	L2
L3	L2 or dna.clm.	17060	L3
L4	L3 and l1	18	L4
L5	dam same (bacter$ or microorgan$ or salmonel$ or shigel$ or coli)	446	L5
L6	dam same (prokaryot$ or procaryot$)	13	L6
L7	L5 not l6 not l4	425	L7
L8	($methylase or methyltransferase$ or methyl-transferase$)	2250	L8
L9	L8 and l7	153	L9
L10	L9 and (heterologous or foreign or nonnative or recombinant or artificial or fusion)	152	L10
L11	L9 and (heterologous or foreign or nonnative or fusion)	121	L11
L12	L9 and (heterologous or foreign or nonnative or fusion)	121	L12
L13	($methylase or methyltransferase$ or methyl-transferase$ or dam) near50 (mutant or mutation or mutagenesis or alter$ or mutants or mutations or insertion or deletion or modification or modified or truncated or trucation)	1690	L13

	fraction)		
L14	L13 and l5	106	L14

END OF SEARCH HISTORY